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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/002,491

DATE: 12/11/2001

TIME: 11:58:54

Input Set : A:\RTS-0239 Sequence Listing.txt

Output Set: N:\CRF3\12112001\I002491.raw

ENTERED

6 <110> APPLICANT: Brett P. Monia
 7 Andrew T. Watt
 9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF FXR EXPRESSION
 11 <130> FILE REFERENCE: RTS-0239
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/002,491
 C--> 13 <141> CURRENT FILING DATE: 2001-11-15
 13 <160> NUMBER OF SEQ ID NOS: 88
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 20
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial Sequence
 21 <220> FEATURE:
 23 <223> OTHER INFORMATION: Antisense Oligonucleotide
 25 <400> SEQUENCE: 1
 26 tccgtcatcg ctctcaggg 20
 29 <210> SEQ ID NO: 2
 30 <211> LENGTH: 20
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Artificial Sequence
 34 <220> FEATURE:
 36 <223> OTHER INFORMATION: Antisense Oligonucleotide
 38 <400> SEQUENCE: 2
 39 atgcattctg cccccaagga 20
 42 <210> SEQ ID NO: 3
 43 <211> LENGTH: 2218
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Homo sapiens
 47 <220> FEATURE:
 49 <220> FEATURE:
 50 <221> NAME/KEY: CDS
 51 <222> LOCATION: (354)...(1772)
 53 <400> SEQUENCE: 3
 54 acgagactct ctctcctcc tcacctcatt gtctccccga cttatcctaa tgcgaaattg 60
 55 gattctgagc atttgtagca aaatcgctgg gatctggaga ggaagactca gtccagaatc 120
 56 ctcccagggc ctgaaagtc catctctgac ccaaaacaat ccaaggaggt agaagacatc 180
 57 gtagaaggag tgaaagaaga aaagaagact tagaaacata gtcaaaagt aacactgctt 240
 58 ctcttagttt cctggatttc ttctggacat ttctcaaga tgaaacttca gacactttgg 300
 59 agtttttttt gaagaccacc ataaagaaag tgcatttcaa ttgaaaaatt tgg atg 356
 60 Met
 61 1
 63 gga tca aaa atg aat ctc att gaa cat tcc cat tta cct acc aca gat 404
 64 Gly Ser Lys Met Asn Leu Ile Glu His Ser His Leu Pro Thr Thr Asp
 65 5 10 15
 67 gaa ttt tct ttt tct gaa aat tta ttt ggt gtt tta aca gaa caa gtg 452
 68 Glu Phe Ser Phe Ser Glu Asn Leu Phe Gly Val Leu Thr Glu Gln Val
 69 20 25 30
 71 gca ggt cct ctg gga cag aac ctg gaa gtg gaa cca tac tcg caa tac 500

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72 Ala Gly Pro Leu Gly Gln Asn Leu Glu Val Glu Pro Tyr Ser Gln Tyr
73      35                      40                      45
75 agc aat gtt cag ttt ccc caa gtt caa cca cag att tcc tcg tca tcc      548
76 Ser Asn Val Gln Phe Pro Gln Val Gln Pro Gln Ile Ser Ser Ser Ser
77 50                      55                      60                      65
79 tat tat tcc aac ctg ggt ttc tac ccc cag cag cct gaa gag tgg tac      596
80 Tyr Tyr Ser Asn Leu Gly Phe Tyr Pro Gln Gln Pro Glu Glu Trp Tyr
81                      70                      75                      80
83 tct cct gga ata tat gaa ctc agg cgt atg cca gct gag act ctc tac      644
84 Ser Pro Gly Ile Tyr Glu Leu Arg Arg Met Pro Ala Glu Thr Leu Tyr
85                      85                      90                      95
87 cag gga gaa act gag gta gca gag atg cct gta aca aag aag ccc cgc      692
88 Gln Gly Glu Thr Glu Val Ala Glu Met Pro Val Thr Lys Lys Pro Arg
89      100                      105                      110
91 atg ggc gcg tca gca ggg agg atc aaa ggg gat gag ctg tgt gtt gtt      740
92 Met Gly Ala Ser Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val Val
93      115                      120                      125
95 tgt gga gac aga gcc tct gga tac cac tat aat gca ctg acc tgt gag      788
96 Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu
97 130                      135                      140                      145
99 ggg tgt aaa ggt ttc ttc agg aga agc att acc aaa aac gct gtg tac      836
100 Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val Tyr
101                      150                      155                      160
103 aag tgt aaa aac ggg ggc aac tgt gtg atg gat atg tac atg cga aga      884
104 Lys Cys Lys Asn Gly Gly Asn Cys Val Met Asp Met Tyr Met Arg Arg
105                      165                      170                      175
107 aag tgt caa gag tgt cga cta agg aaa tgc aaa gag atg gga atg ttg      932
108 Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Lys Glu Met Gly Met Leu
109      180                      185                      190
111 gct gaa tgc ttg tta act gaa att cag tgt aaa tct aag cga ctg aga      980
112 Ala Glu Cys Leu Leu Thr Glu Ile Gln Cys Lys Ser Lys Arg Leu Arg
113      195                      200                      205
115 aaa aat gtg aag cag cat gca gat cag acc gtg aat gaa gac agt gaa      1028
116 Lys Asn Val Lys Gln His Ala Asp Gln Thr Val Asn Glu Asp Ser Glu
117 210                      215                      220                      225
119 ggt cgt gac ttg cga caa gtg acc tcg aca aca aag tca tgc agg gag      1076
120 Gly Arg Asp Leu Arg Gln Val Thr Ser Thr Thr Lys Ser Cys Arg Glu
121                      230                      235                      240
123 aaa act gaa ctc acc cca gat caa cag act ctt cta cat ttt att atg      1124
124 Lys Thr Glu Leu Thr Pro Asp Gln Gln Thr Leu Leu His Phe Ile Met
125                      245                      250                      255
127 gat tca tat aac aaa cag agg atg cct cag gaa ata aca aat aaa att      1172
128 Asp Ser Tyr Asn Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys Ile
129      260                      265                      270
131 tta aaa gaa gaa ttc agt gca gaa gaa aat ttt ctc att ttg acg gaa      1220
132 Leu Lys Glu Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr Glu
133      275                      280                      285
135 atg gca acc aat cat gta cag gtt ctt gta gaa ttc aca aaa aag cta      1268
136 Met Ala Thr Asn His Val Gln Val Leu Val Glu Phe Thr Lys Lys Leu

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```

137 290          295          300          305
139 cca gga ttt cag act ttg gac cat gaa gac cag att gct ttg ctg aaa 1316
140 Pro Gly Phe Gln Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu Lys
141          310          315          320
143 ggg tct gcg gtt gaa gct atg ttc ctt cgt tca gct gag att ttc aat 1364
144 Gly Ser Ala Val Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe Asn
145          325          330          335
147 aag aaa ctt ccg tct ggg cat tct gac cta ttg gaa gaa aga att cga 1412
148 Lys Lys Leu Pro Ser Gly His Ser Asp Leu Leu Glu Glu Arg Ile Arg
149          340          345          350
151 aat agt ggt atc tct gat gaa tat ata aca cct atg ttt agt ttt tat 1460
152 Asn Ser Gly Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe Tyr
153          355          360          365
155 aaa agt att ggg gaa ctg aaa atg act caa gag gag tat gct ctg ctt 1508
156 Lys Ser Ile Gly Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu Leu
157 370          375          380          385
159 aca gca att gtt atc ctg tct cca gat aga caa tac ata aag gat aga 1556
160 Thr Ala Ile Val Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp Arg
161          390          395          400
163 gag gca gta gag aag ctt cag gag cca ctt ctt gat gtg cta caa aag 1604
164 Glu Ala Val Glu Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln Lys
165          405          410          415
167 ttg tgt aag att cac cag cct gaa aat cct caa cac ttt gcc tgt ctc 1652
168 Leu Cys Lys Ile His Gln Pro Glu Asn Pro Gln His Phe Ala Cys Leu
169          420          425          430
171 ctg ggt cgc ctg act gaa tta cgg aca ttc aat cat cac cac gct gag 1700
172 Leu Gly Arg Leu Thr Glu Leu Arg Thr Phe Asn His His His Ala Glu
173          435          440          445
175 atg ctg atg tca tgg aga gta aac gac cac aag ttt acc cca ctt ctc 1748
176 Met Leu Met Ser Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu Leu
177 450          455          460          465
179 tgt gaa atc tgg gac gtg cag tga tggggattac aggggagggg tctagctcct 1802
180 Cys Glu Ile Trp Asp Val Gln
181          470
182 ttttctctct catattaatc tgatgtataa ctttccttta tttcacttgt acccagtttc 1862
183 actcaagaaa tcttgatgaa tatttatgtt gtaattacat gtgtaacttc cacaactgta 1922
184 aatattgggc tagatagaac aactttctct acattgtgtt ttaaaaggct ccagggaatc 1982
185 ctgcattcta attggcaagc cctgtttgcc taattaaatt gattgttact tcaattctat 2042
186 ctgttgaact agggaaaatc tcattttgct catcttacca tattgcatat attttattaa 2102
187 agagttgtat tcaatcttgg caataaagca aacataatgg caacagaaaa aaaaaaaaaa 2162
188 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2218
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 27
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
197 <223> OTHER INFORMATION: PCR Primer
199 <400> SEQUENCE: 4
200 tcagtgtaaa tctaagcgac tgagaaa 27

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```

203 <210> SEQ ID NO: 5
204 <211> LENGTH: 23
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
210 <223> OTHER INFORMATION: PCR Primer
212 <400> SEQUENCE: 5
213 gcaagtcacg accttcactg tct                                     23
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 27
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
223 <223> OTHER INFORMATION: PCR Probe
225 <400> SEQUENCE: 6
226 agcagcatgc agatcagacc gtgaatg                                   27
229 <210> SEQ ID NO: 7
230 <211> LENGTH: 19
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
236 <223> OTHER INFORMATION: PCR Primer
238 <400> SEQUENCE: 7
239 gaaggtgaag gtcggagtc                                           19
242 <210> SEQ ID NO: 8
243 <211> LENGTH: 20
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
249 <223> OTHER INFORMATION: PCR Primer
251 <400> SEQUENCE: 8
252 gaagatggtg atgggatttc                                           20
255 <210> SEQ ID NO: 9
256 <211> LENGTH: 20
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
262 <223> OTHER INFORMATION: PCR Probe
264 <400> SEQUENCE: 9
265 caagcttccc gttctcagcc                                           20
268 <210> SEQ ID NO: 10
269 <211> LENGTH: 91000
270 <212> TYPE: DNA
271 <213> ORGANISM: Homo sapiens
273 <220> FEATURE:
275 <221> NAME/KEY: misc_feature
276 <222> LOCATION: 73772-74071
277 <223> OTHER INFORMATION: n = A,T,C or G
279 <221> NAME/KEY: intron

```

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```

280 <222> LOCATION: (576)...(19018)
281 <223> OTHER INFORMATION: intron 1
283 <221> NAME/KEY: intron
284 <222> LOCATION: (19154)...(19785)
285 <223> OTHER INFORMATION: intron 2
287 <221> NAME/KEY: intron
288 <222> LOCATION: (19919)...(37293)
289 <223> OTHER INFORMATION: intron 3
291 <221> NAME/KEY: intron
292 <222> LOCATION: (37660)...(58973)
293 <223> OTHER INFORMATION: intron 4
295 <221> NAME/KEY: intron
296 <222> LOCATION: (59115)...(61405)
297 <223> OTHER INFORMATION: intron 5
299 <221> NAME/KEY: intron
300 <222> LOCATION: (61540)...(63027)
301 <223> OTHER INFORMATION: intron 6
303 <221> NAME/KEY: intron
304 <222> LOCATION: (63127)...(63463)
305 <223> OTHER INFORMATION: intron 7
307 <221> NAME/KEY: intron
308 <222> LOCATION: (63564)...(67187)
309 <223> OTHER INFORMATION: intron 8
311 <221> NAME/KEY: intron
312 <222> LOCATION: (67335)...(87922)
313 <223> OTHER INFORMATION: intron 9
315 <221> NAME/KEY: intron
316 <222> LOCATION: (88037)...(89288)
317 <223> OTHER INFORMATION: intron 10
320 <400> SEQUENCE: 10
321 tgatatgggt ggctgggcag agggaagggt caaaaaggct cccagcttct agttcagtc 60
322 cggggaagtg atagagctat tcaaagaagt tgtagtgaga gagagggaag atgacagttt 120
323 ggttttagtt gatgtgtaca gaaatacggg tgcccaggag cccacaaaac ggccagagga 180
324 gaaatgcttt caaaggcaag ctgcagggct ccttggtttt gtcacattcc tcattctggg 240
325 gctttgcggt tttgtcttgg gaatctcgag gctctcccaa ggttcctttc tatgtttata 300
326 tcatttagca ggggaaggatt gttaatgact aatctgtgtc catgaggcac agagccaagg 360
327 aagagatgct gctgctagcc cagaaggccg cctgtgatca tgcacagtac actggaactc 420
328 tctctcctc ctcacctcat tgtctccccg acttatacta atgcgaaatt ggattctgag 480
329 cattgttagc aaaatcgctg ggatctggag aggaagactc agtccagaat cctcccaggg 540
330 ccttgaaagt ccattctctga cccaaaacaa tccaagtaag tacctaattc ctttgggagt 600
331 gggttgtgta tctcacagca acagagaaaa aatagtcact taaaagtttc tctttgacat 660
332 ctgtaatgta tgtcaataaa tgaattctaa gttagtagag tttgatgtaa agtcctgaaa 720
333 attaaaaaag agagaaacta aaaaacaaa agaagcagaa gcaaaagtta atgagtccta 780
334 acagttgctt acctattgaa aacttattta gaaatactct ttaacattg tggtcacctg 840
335 agtaaatc ac tggagatagt gcatttcaga aatgtctccg ttctgattcc ataaacaatt 900
336 tgacttgat agtgtgctat attttggtga tttatcaaat cttgatgtga gtttgggagt 960
337 attgctaata tcagatgact tgggaactaa gaataagaca ttaaacctat gcttaattga 1020
338 aatgaaattt ttcctagaa gaagagtagg tggaaaaagt cttctttctt gaattcagtt 1080
339 gtaaaactct ctattgcttt ccattttgaa tattaatatg acaggaaata tcagatggaa 1140

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10